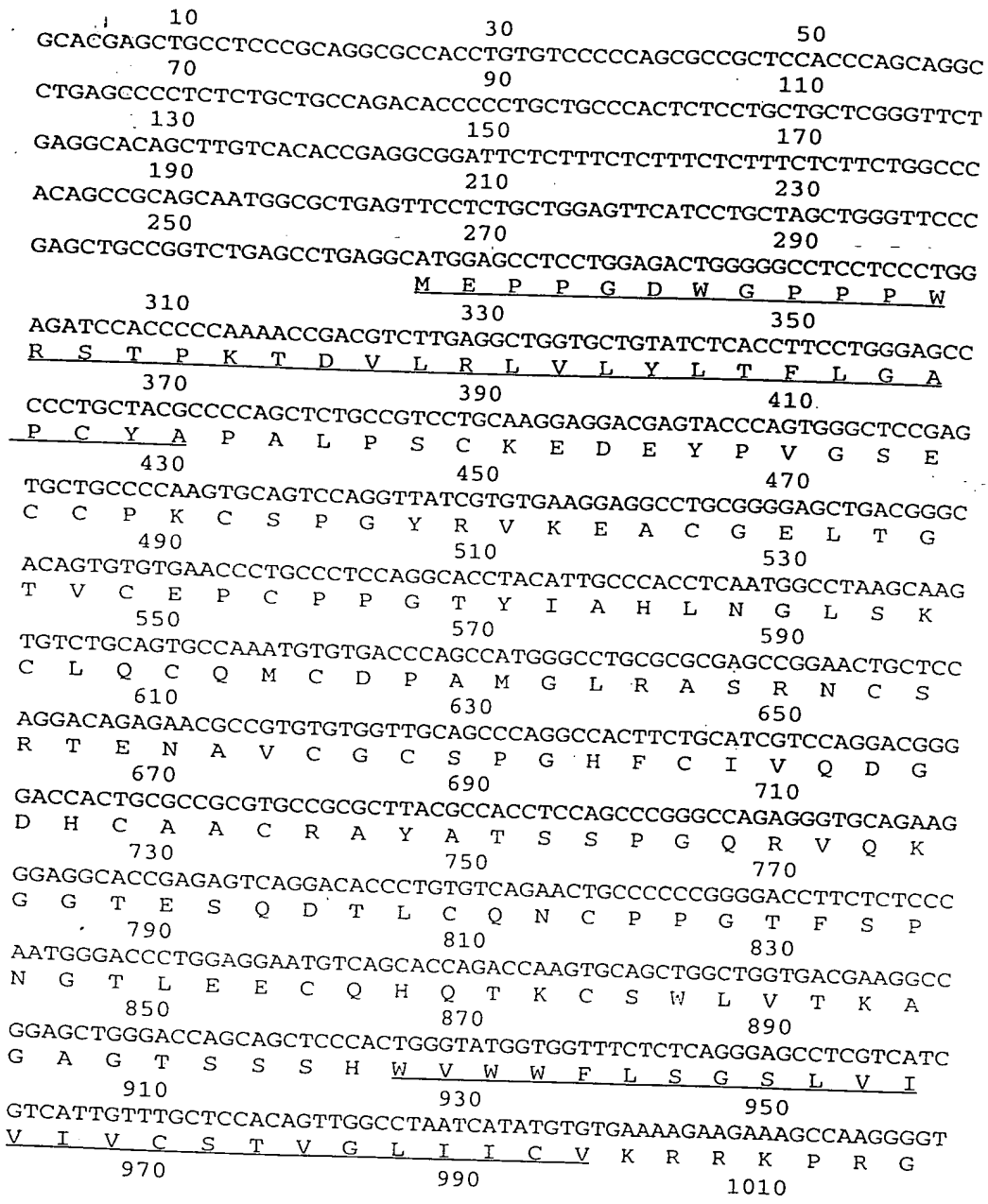
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30
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70
90
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150
170
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190
210
230
ACAGCCGCAGCAATGGCGCTGAGTTCCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCC
250
270
290
GAGCTGCCGGTCTGAGCCTGAGGCATGGAGCCTCCTGGAGACTGGGGGCCTCCTCCCTGG
M E P P G D W G P P P W
310
330
350
AGATCCACCCCCAAAACCGACGTCTTGAGGCTGGTGCTGTATCTCACCTTCCTGGGAGCC
R S T P K T D V L R L V L Y L T F L G A
370
390
410
CCCTGCTACGCCCCAGCTCTGCCGTCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAG
P C Y A P A L P S C K E D E Y P V G S E
430
450
470
TGCTGCCCCAAGTGCAGTCCAGGTTATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGC
C C P K C S P G Y R V K E A C G E L T G
490
510
530
ACAGTGTGTGAACCCTGCCCTCCAGGCACCTACATTGCCCACCTCAATGGCCTAAGCAAG
T V C E P C P P G T Y I A H L N G L S K
550
570
590
TGTCTGCAGTGCCAAATGTGTGACCCAGCCATGGGCCTGCGCGCGAGCCGGAACTGCTCC
C L Q C Q M C D P A M G L R A S R N C S
610
630
650
AGGACAGAGAACGCCGTGTGTGGTTGCAGCCCAGGCCACTTCTGCATCGTCCAGGACGGG
R T E N A V C G C S P G H F C I V Q D G
670
690
710
GACCACTGCGCCGCGTGCCGCGCTTACGCCACCTCCAGCCCGGGCCAGAGGGTGCAGAAG
D H C A A C R A Y A T S S P G Q R V Q K
730
750
770
GGAGGCACCGAGAGTCAGGACACCCTGTGTCAGAACTGCCCCCCGGGGACCTTCTCTCCC
G G T E S Q D T L C Q N C P P G T F S P
790
810
830
AATGGGACCCTGGAGGAATGTCAGCACCAGACCAAGTGCAGCTGGCTGGTGACGAAGGCC
N G T L E E C Q H Q T K C S W L V T K A
850
870
890
GGAGCTGGGACCAGCAGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATC
G A G T S S S H W V W W F L S G S L V I
910
930
950
GTCATTGTTTGCTCCACAGTTGGCCTAATCATATGTGTGAAAAGAAGAAAGCCAAGGGGT
V I V C S T V G L I I C V K R R K P R G
970
990
1010

Figure 1A

GATGTAGTCAAGGTGATCGTCTCCGTCCAGCGGAAAAGACAGGAGGCAGAAGGTGAGGCC
D V V K V I V S V Q R K R Q E A E G E A
1030 1050 1070
ACAGTCATTGAGGCCCTGCAGGCCCCTCCGGACGTCACCACGGTGGCCGTGGAGGAGACA
T V I E A L Q A P P D V T T V A V E E T
1090 1110 1130
ATACCCTCATTCACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCACCCCGACGC
I P S F T G R S P N H *
1150 1170 1190
CAGAGATACCTGGAGCGACGGCTGAATGAAAGAGGCTGTCCACCTGGCGGAACCACCGGA
1210 1230 1250
GCCCGGAGGCTTGGGGGCTCCACCCTGGACTGGCTTCCGTCTCCTCCAGTGGAGGGAGAG
1270 1290 1310
GTGGCGCCCCTGCTGGGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGGGCCAGTGAG
1330 1350 1370
GGCCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCCTGAGGAGGAGCGCCA
1390 1410 1430
GTTGCCCCTCGCTCACAGACCACACACCCAGCCCTCCTGGGCCAACCCAGAGGGCCTTCA
1450 1470 1490
GACCCCAGCTGTGTGCGCGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTG
1510 1530 1550
CCTCACAGCCAAGGCTGGACTGGGTTGGCTGCAGTGTGGTGTTTAGTGGATACCACATCG
1570 1590 1610
GAAGTGATTTTCTAAATTGGATTTGAATTCGGCTCCTGTTTTCTATTTGTCATGAAACAG
1630 1650 1670
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1690
AAAAAAAAAAAAAAAAAAAAAAA

Figure 1B

Percent Similarity: 46.591 Percent Identity: 28.788

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    ...: ||. .:. | .:.. .. ..|.:.:|  :
  1 ..............MVSLPRLCALWGCLLTAVHLGQCVTCSDKQYLHD 34

 51 SECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCD 100
    ::||. | || |:.. |..|. | |.||..|.: |::|   :| | . |:
 35 GQCCDLCQPGSRLTSHCTALEKTQCHPCDSGEFSAQWNREIRCHQHRHCE 84

101 PAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQRV 150
    |. |||..:.:.. ..:.||.|..|: |. .|   |.|| ....: ||  |
 85 PNQGLRVKKEGTAESDTVCTCKEGQHCTSKD...CEACAQHTPCIPGFGV 131

151 QKGGTESQDTLCQNCPPGTFSPNGTL.EECQHQTKC.SWLVTKAGAGTSS 198
  . :||. ||:|: ||.| || .:.| |.| . |.| .. :.  . |||
132 MEMATETTDTVCHPCPVGFFSNQSSLFEKCYPWTSCEDKNLEVLQKGTSQ 181

199 SH.......WVWWFLSGSLVIVIVCSTVGLIICVKR..RKPRGDVVKVIV 239
    .:      ::: :|  .:|:.|:....|:::::|:  :||::: : . .
182 TNVICGLKSRMRALLVIPVVMGILITIFGVFLYIKKVVKKPKDNEMLPPA 231

240 SVQRKRQEAEG......EATVIEALQAPPDVTTVAVEETIPSFTGRSPNH 283
    . ....|| |:      .|.| |.|:::..|| ...|.  |. :| ...
232 ARRQDPQEMEDYPGHNTAAPVQETLHGCQPVTQEDGKESRISVQERQVTD 281
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Figure 2

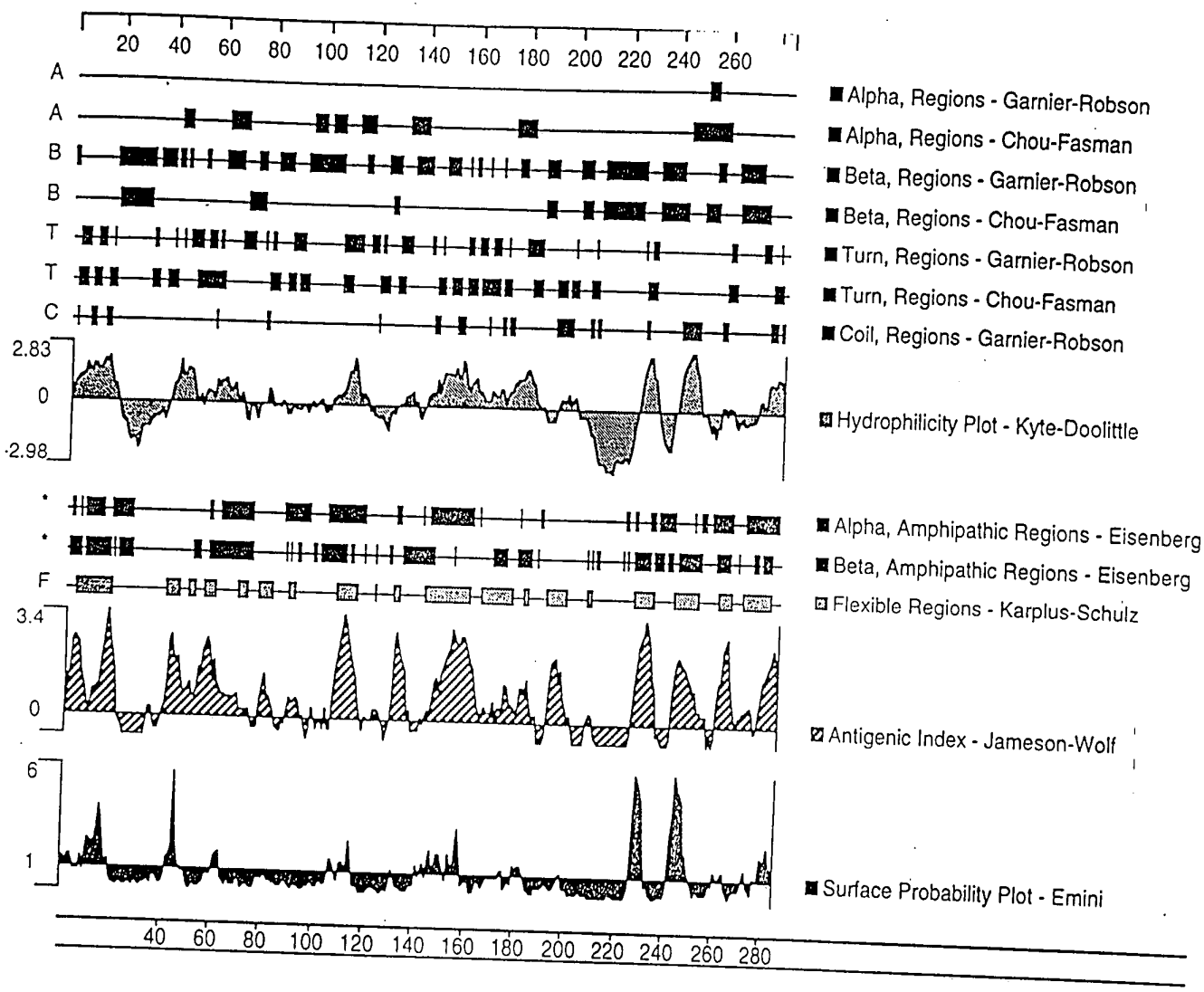
20 40 60 80 100 120 140 160 180 200 220 240 260
A
A
B
B
T
T
C
2.83
0
-2.98
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
Hydrophilicity Plot - Kyte-Doolittle
F
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
Flexible Regions - Karplus-Schulz
3.4
0
Antigenic Index - Jameson-Wolf
6
1
Surface Probability Plot - Emini
40 60 80 100 120 140 160 180 200 220 240 260 280

Figure 3

```
          10                  30                  50
CCCCCTTCTACAGGAAACCCGGAGTGGACTGGAACGGTGCAGGGGGAGAACTCGCCCCTC
          70                  90                  110
CCATCGGGCGCCTCCTTCATACCGGCCCTTCCCCTCGGCTTTGCCTGGACAGCTCCTGCC
          130                 150                 170
TCAGGCAGCGCCACCTGTGTCGCCCAGCGCCGCTCCACCCAGCAGGCCTGAGCCCCTCTC
          190                 210                 230
TGCTGCCAGACACCCCCTGCTGCCCACTACTCCTGCTGCTCGGGTTCTGAGGCACAGCTT
          250                 270                 290
GTCACACCGAGGCGGATTCTCTTTCTCTTTCTCTTTCTCTTCTGGCCCACAGCCGCAGCA
          310                 330                 350
ATGGCGCTGAGTTCCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCCGAGCTGCCGGTC
          370                 390                 410
TGAGCCTGAGTCATGGAGCCTCCTGGAGACTGGGGGCCTCCTCCCTGGAGATCCACCCCC
                M  E  P  P  G  D  W  G  P  P  P  W  R  S  T  P
          430                 450                 470
AGAACCGACGTCTTGAGGCTGGTGCTGTATCTCACCTTCCTGGGAGCCCCCTGCTACGCC
R  T  D  V  L  R  L  V  L  Y  L  T  F  L  G  A  P  C  Y  A
          490                 510                 530
CCAGCTCTGCCGTCCTGCAAGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAG
P  A  L  P  S  C  K  E  D  E  Y  P  V  G  S  E  C  C  P  K
          550                 570                 590
TGCAGTCCAGGTTATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGCACAGTGTGTGAA
C  S  P  G  Y  R  V  K  E  A  C  G  E  L  T  G  T  V  C  E
          610                 630                 650
CCCTGCCCTCCAGGCACCTACATTGCCCACCTCAATGGCCTAAGCAAGTGTCTGCAGTGC
P  C  P  P  G  T  Y  I  A  H  L  N  G  L  S  K  C  L  Q  C
          670                 690                 710
CAAATGTGTGACCCAGATATTGGTTCCCCCTGTGACCTCAGGGGAAGAGGTCACCTGGAG
Q  M  C  D  P  D  I  G  S  P  C  D  L  R  G  R  G  H  L  E
          730                 750                 770
GCTGGTGCCCACCTGAGTCCAGGCAGACAGAAAGGGGAACCAGACCCAGAGGTGGCCTTT
A  G  A  H  L  S  P  G  R  Q  K  G  E  P  D  P  E  V  A  F
          790                 810                 830
GAGTCACTGAGCGCAGAGCCTGTCCATGCGGCCAACGGCTCTGTCCCCTTGGAGCCTCAT
E  S  L  S  A  E  P  V  H  A  A  N  G  S  V  P  L  E  P  H
          850                 870                 890
GCCAGGCTCAGCATGGCCAGTGCTCCCTGCGGCCAGGCAGGACTGCACCTGCGGGACAGG
A  R  L  S  M  A  S  A  P  C  G  Q  A  G  L  H  L  R  D  R
          910                 930                 950
GCTGACGGCACACCTGGGGGCAGGGCCTGAGCCTACAGGGAGGCACAGGGCAGGTGGGCT
A  D  G  T  P  G  G  R  A  *
          970                 990                 1010
AGCCATGAACAGAAGAGGAAGCTGGAGTGCTTTGGGGGTTCATGCATGTAGGCTGGGATT
```

Figure 4A

1030 1050 1070
TGGGGCTCACACCTCAACCTGCATGCCCAGTTCCATGCCCCTCCCCTCTTGTGAAAGCAC
1090 1110 1130
CTGTCTACTTGGGCTGAGGATGTGGGGCACAGGTGGCAGGTGAGGCTGCCCTCAGGAGG
1150 1170 1190
GGCCCAGGCCCAGCTTGTACCCCACCTCCACCAGTACCTGAAGAAGTGGGGCTCTCACCC
1210 1230 1250
TACCTGCCTCTGCCATTGGAATGGCCTGGTTTGCACAGATGGGAAACCCGTTTGAGGGGT
1270 1290 1310
GGGTGTCTGGGTGGGCACGTGGGGCGAGGACCTGCCTGAGGGACCCTGCCCTGGAACTGA
1330 1350 1370
CAGTGCAAGCTCGGCGTCCTGCCCATCTGGGCAGAAGGCTGGTTTCTCCCATCAACGAAG
1390 1410 1430
CCCTCCCAGGACCTTCCTGCAAGCCCTCGTCCCACACGCAGCTCTGCCGTCCCTTGGTGT
1450 1470 1490
CCCTCCCGGCCTCAGGTCCTCCATGCTGGGTACCTCTGGGCACCTCGTTTGGCTGAGCCA
1510 1530 1550
GGGGTTCAGCCTGGCAGGGCGCCCTGGCAGCAGTCCTTGGCCTGTGGATGCTGTCCTGGC
1570 1590 1610
CTGTGGATGGTGTCCCGCCCTCCACGTACCCCTCTCACCCCCTCCTCTTGGACTCCAGCC
1630 1650 1670
ATGGGCCTGCGCGCGAGCCGGAACTGCTCCAGGACAGAGAACGCCGTGTGTGGCTGCAGC
1690 1710 1730
CCAGGCCACTTCTGCATCGTCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTTACGCC
1750 1770 1790
ACCTCCAGCCCGGGCCAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAGGACACCCTGTGT
1810 1830 1850
CAGAACTGCCCCCCGGGGACCTTCTCTCCCAATGGGACCCTGGAGGAATGTCAGCACCAG
1870 1890 1910
ACCAATTGGCCTAATCATATGTGTGAAAAGAAGAAAGCCAAGGGGTGAGCACACGGTGGC
1930 1950 1970
CCCATCAGGGTTCATGTCCCCAGCCGTCACCTCTTGGAGCTCTGTCACCCCAAGCCTGGG
1990 2010 2030
AGGTGGCCCCAGAGCTTTTCCAGGATCCGCGGCTCCTCCCAGGGCAGCCACTGCAGGCTG
2050 2070 2090
GGGCAGGTGTATGTAGTCAAGGTGATCGTCTCCGTCCAGCGGTAAAAGACAGGAGGCAGA
2110 2130 2150
AGGTGAGGCCACAGTCATTGAGCCCTGCAGGCCCCTCCGGACGTCACCACGGTGGCCGTG
2170 2190 2210
GAGGAGACAATACCCTCATTCACGGGGAGGAGCCCAAACCACTGACCCACAGACTCTGCA
2230 2250 2270
CCCCGACGCCAGAGATACCTGGAGAGACGGCTGCTGATAGAGGCTGTCCACCTGGCGAAA
2290 2310 2330
CCACCGGAGCCCGGAGGCTTGGGGGCTCCGCCCTGGGCTGGTTTCCGTCTCCTCCAGTGG
2350 2370 2390
AGGGAGAGGTGGTGCCCCTGCTGGTGGTAGAGCTGGGGACGCCACGTGCCATTCCCATGG
2410 2430 2450
TTCAGTGAGGGGCTGGTGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCCAGAGTCCTGAGG
2470 2490 2510
AGGAGCCCCAGTTGCCCCTCGCTCACAGACCACACACCCAGCCCTCCTGGGCCAACCCAG
2530 2550 2570
AGGCCCCTTCAGACCCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCTCAGCAGGACAGGC
2590 2610 2630
CCCGGGCACTGCCTCACAGCCAAGGCTGGAATGGGTTGGCTGCAGTGTGGTGTTTAGTGG
2650 2670 2690
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Figure 4B

Percent Similarity: 47.541   Percent Identity: 24.590

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    |.|.: |:: :    . :...  |.  :.|  .|: :.: ..|:  ||  .
  1 MAPVAVWAALAVGLELWAAAHALPAQVAF..TPYAPEPGSTCRLREYYDQ  48

 49 VGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQM  98
    .:  ||.|||||  :.|   |..  .:|||:.|..:||.. :|  :..|| |.
 49 TAQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGS  98

 99 ..CDPDIGSPCDLRGRGHL.............EAGAHLSPGRQKGEPDPE 133
     :.:::...  |:..::               :.|.:|::. .|. |: :
 99 RCSSDQVETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFG 148

134 VA..............................FESLSAEPVHAANGS 150
    ||                              : .: | |.:|. :.
149 VARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDA 198

151 VPLEPHARLSMASAPC..GQAGLHLRDRADGTPGGRA............. 185
    |. .. :   |||.::.  .|:.   .::.:.||:...
199 VCTSTSPTRSMAPGAVHLPQPVSTRSQHTQPTPEPSTAPSTSFLLPMGPS 248
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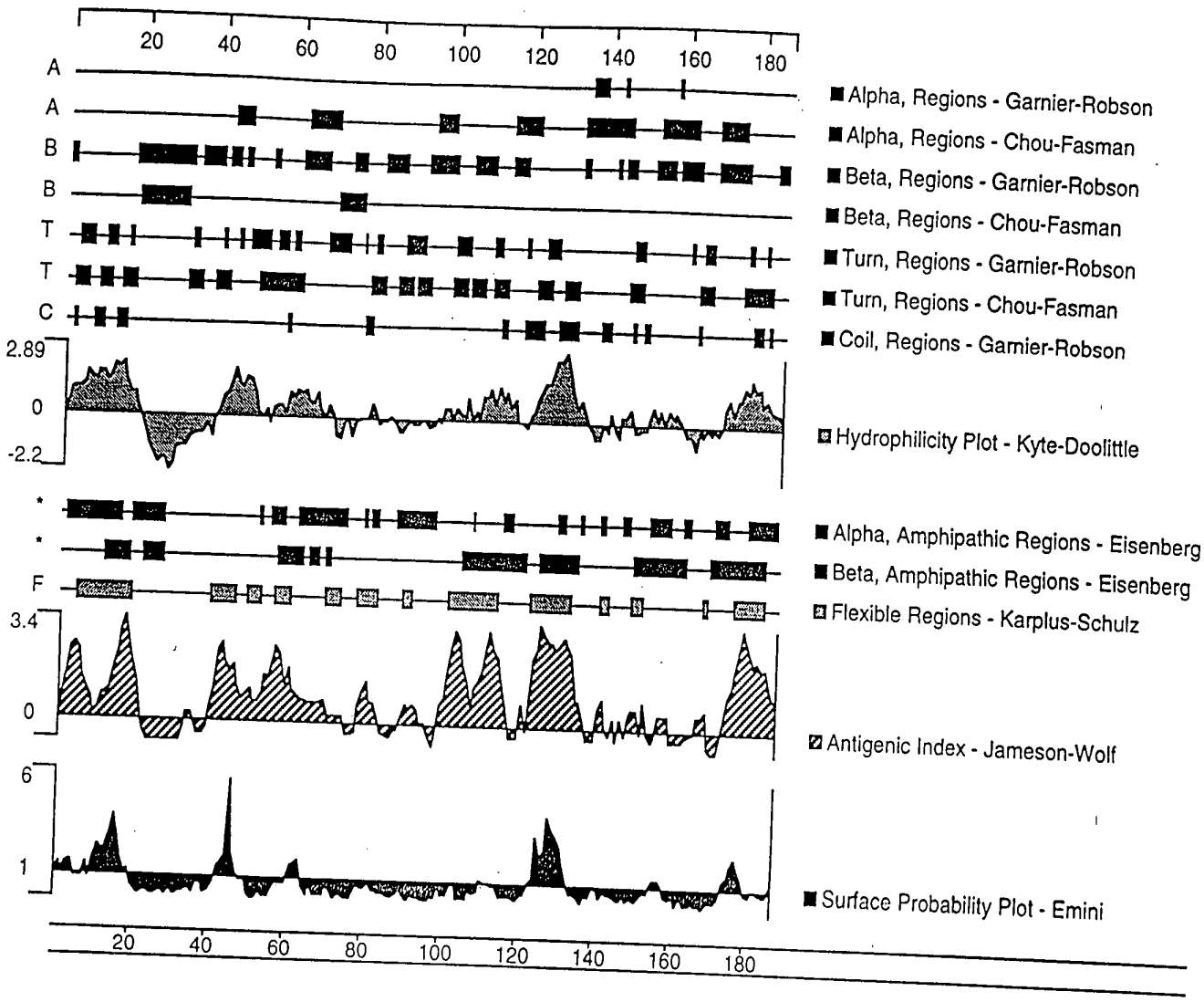
Figure 5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40
60
80
100
120
140
160
180
A
A
B
B
T
T
C
Alpha, Regions - Garnier-Robson
Alpha, Regions - Chou-Fasman
Beta, Regions - Garnier-Robson
Beta, Regions - Chou-Fasman
Turn, Regions - Garnier-Robson
Turn, Regions - Chou-Fasman
Coil, Regions - Garnier-Robson
2.89
0
-2.2
Hydrophilicity Plot - Kyte-Doolittle
*
*
F
Alpha, Amphipathic Regions - Eisenberg
Beta, Amphipathic Regions - Eisenberg
Flexible Regions - Karplus-Schulz
3.4
0
Antigenic Index - Jameson-Wolf
6
1
Surface Probability Plot - Emini

Figure 6

```
          10                  30                  50
AAAGCTCGGGCTCCACCGGGGACGACCGCTCCTAGAAACTGAGTGGTATCCCCCGGGCCT
          70                  90                 110
GCAGGAATTCCAACCTGCCTGAAGGGACCCTGCCCTGGAACTGACAGTGCAAGCTCGGCG
         130                 150                 170
TCCTGCCCATCTGGGAAGAAGGCTGGTTTCTCCCATCAACGAAGCCCTCCCAGGACCTTC
         190                 210                 230
CTGCAAGCCCTCGTCCCACACGCAGCTCTGCCGTCCCTTGGTGTCCCTCCCGGCCTCAGG
         250                 270                 290
TCCTCCATGCTGGGTACCTCTGGGCACCTCGTTTGGCTGAGCCAGGGGTTCAGCCTGGCA
       M   L   G   T   S   G   H   L   V   W   L   S   Q   G   F   S   L   A
         310                 330                 350
GGGCGCCCTGGCAGCAGTCCTTGGCCTGTGGATGCTGTCCTGGCCTGTGGATGGTGTCCC
G   R   P   G   S   S   P   W   P   V   D   A   V   L   A   C   G   W   C   P
         370                 390                 410
GGCCTCCACGTACCCCCTCTCAGCCCCTCCTCTTGGACTCCAGCCATGGGCCTGCGCGCG

G   L   H   V   P   P   L   S   P   S   S   W   T   P   A   M   G   L   R   A
         430                 450                 470
AGCCGGAACTGCTCCAGGACAGAGAACGCCGTGTGTGGCTGCAGCCCAGGCCACTTCTGC
S   R   N   C   S   R   T   E   N   A   V   C   G   C   S   P   G   H   F   C
         490                 510                 530
ATCGTCCAGGACGGGGACCACTGCGCCGCGTGCCGCGCTTACGCCACCTCCAGCCCGGGC
I   V   Q   D   G   D   H   C   A   A   C   R   A   Y   A   T   S   S   P   G
         550                 570                 590
CAGAGGGTGCAGAAGGGAGGCACCGAGAGTCAGGACACCCTGTGTCAGAACTGCCCCCGG
Q   R   V   Q   K   G   G   T   E   S   Q   D   T   L   C   Q   N   C   P   R
         610                 630                 650
GGACCTTCTCTCCCAATGGGACCCTGGAGGAATGTCAGCACCAGACCAAGTAAGTGAACC
G   P   S   L   P   M   G   P   W   R   N   V   S   T   R   P   S   K   *
         670                 690                 710
CGGGGGAGGCCAGCTCTGTGCCCTGGGGAGGGGGCTCCACGTTGCTTCCCTGGGAGATGA
         730                 750                 770
CCGTCTTCTCCAGCAGAAAGGTTGAAGGTCCCACCCTGAGCGGCACCCTGGTCACATGCC
         790                 810                 830
TGCGTCCAGGAGAGCTGCAGGGTGAAGCCTGTGTGCCCCAGATAACCCCTTCCATGGGCC
         850                 870                 890
CAGACAAAGCCTCATCAGATCTGAGCTTCCTGGAGGCTCAGGATGGGCCTTCCCAGAAGC
         910                 930                 950
AGGCCCAGAGGGAGGCTGCCTCCAGATCCCCTGTCCCCTGGGGCTGTGGGTGTCCCTGAA
         970                 990                1010
TGTCAGGGCCATGGGAGGGCCCCTGGGCTTCAGGGGTTGGGGAAAGTGAACACTCTGCTC
        1030                1050                1070
TTTGTCCACCTTCGGGAGGACAACCTTCAAATGCTGACCCTGGGCCCCTAACTGACCTGA
        1090                1110                1130
GACTTCAGAGCTTCTTGGGAGGAGCTGGGGTCCCCCAGCGGAGCCTGGGATGGAGCAGGG
        1150                1170                1190
ATGGCTGCCCCAGGGAGGGGGCGGTGGGGCCTTCCATCCTGCTCTGCCCTCCTCGTCCTC
        1210                1230                1250
TGGCCCCAGCTCAGTCCTGTCCATCTCCAGCTCTAACCATTTGTGGCCCGACACTGGCTC
        1270                1290                1310
TCCCTCTACCTTCTGTCCTTGTCTGACACTGGTCTCCCGTGCTCTGGGGTCTCTGCACTG
        1330                1350                1370
ATGGCTGCCTCCCGCTTCTCTCCCCTCTCCCTCTGCCGTCCTGTCTCCTGTGGCCAGTCT
```

Figure 7A

```
      1390                 1410                 1430
CTCCTTGTTTCTCTTCTCCTCCTTCCTTCTCTCCACCTCCCCATAGCCGAGCTTGGAAAA
      1450                 1470                 1490
GTCAGACAGACCTCTGAGGTCTCATCCTGGAGCTGCCACCAGCCCAGCCTCCCTGGGACC
      1510                 1530                 1550
TGTCTTCACTGCCTGGGGCCCTGGGAGCCAGGGAGGCTCCCTGAGGCTGAGTGAACACTG
      1570                 1590                 1610
GGCGCTGCACCTGCCTCTCCCACGTCCTCGGCCCCACTCCCGCAGGTGCAGCTGGCTGGT
      1630                 1650                 1670
GACGAAGCCCGGAGCTGGGACCAGCAGCTCCCACTGGGTATGGTGGTTTCTCTCAGGGAG
      1690                 1710                 1730
CCTCGTCATCGTCATTGTTTGCTCCACAGTTGGCCTAATCATATGTGTGAAAAGAAGAAA
      1750                 1770                 1790
GCCAAGGGGTGATGTAGTCAAGGTGATCGTCTCCGTCCAGGTATTGATCCTCCTCCCCCT
      1810                 1830                 1850
CTCCCTCCCCCCTCCACCTTCCCACCTCCCCTCTCCCCGCTGGGGCTGGTGTTTCTGGTG
      1870                 1890                 1910
TACATGGTGGGGGCTCCCAGTTCTCTGAGGGTCCTGAGTCTTTCAAGTACAGCCACGGTA
      1930                 1950                 1970
GCTCAGGAAAGAACCCACCCCCTCAAACTGAAAGCAGTAAAATGAACCCGAGAACCTGGA
      1990                 2010                 2030
GTCCCAGGGGGGCCTGAGCAGGCAGGGTCTCCACGATTCGTGTGCTCACAGCGGGAAAAG
      2050                 2070                 2090
ACAGGAGGCAGAAGGTGAGGCCACAGTCATTGAGGCCCTGCAGGCCCCTCCGGACGTCAC
      2110                 2130                 2150
CACGGTGGCCGTGGAGGAGACAATACCCTCATTCACGGGGGAGGAGCCCAAACCACTGAC
      2170                 2190                 2210
CCACAGACTCTGCACCCCGACGCCAGAGATACCTGGAGCGACGGCTGCTGAAAGAGGCTG
      2230                 2250                 2270
TCCACCTGGCGAAACCACCGGAGCCCGGAGGTTTGGGGGCTCCGCCCTGGGCTGGTTTCC
      2290                 2310                 2330
GTCTCCTCCAGTGGAGGGAGAGGTGGGGCCCCTGCTGGGGTAGAGCTGGGGACGCCACGT
      2350                 2370                 2390
GCCATTCCCATGGGCCAGTGAGGGCCTGGGGCCTCTGTTCTGCTGTGGCCTGAGCTCCCC
      2410                 2430                 2450
AGAGTCCTGAGGAGGAGCGCCAGTTGCCCCTCGCTCACAGACCACACACCCAGCCCTCCT
      2470                 2490                 2510
GGGTCCAGCCCAGAGGGCCCTTCAGACCCCAGCTGTCTGCGCGTCTGACTCTTGTGGCCT
      2530                 2550                 2570
CAGCAGGACAGGCCCCGGGCACTGCCTTCAAGCCAAGGCTGGACTGGGTTGGCTGCAGTG
      2590                 2610                 2630
TGGTGTTTAGTGGATACCACATCGGAAGTGATTTTCTAAATTGGATTTGAAAAAAAA
```

Figure 7B

Percent Similarity: 45.522 Percent Identity: 26.866

```
  1 MLGTSGHLVWLSQGFSL.................AGRPGSSPWPVD..... 29
    ::. : :. |. |:.|                   |. |||..:  :
  1 .MAPVAVWAALAVGLELWAAAHALPAQVAFTPYAPEPGSTCRLREYYDQT 49

 30 AVLACGWC.PGLHV.........................PPLSPSSW 50
    | :.|:.| || |.                         ..||.:|:
 50 AQMCCSKCSPGQHAKVFCTKTSDTVCDSCEDSTYTQLWNWVPECLSCGSR 99

 51 TPAMGLRASRNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQR 100
    ... .: ....|.|.:| :|.|.|| :| : ..: |  | :. .:.||
100 CSSDQV.ETQACTREQNRICTCRPGWYCALSKQEGCRLCAPLRKCRPGFG 148

101 VQKGGTESQDTLCQNCPRGPSLPMGPWRNVSTRPSK.............. 136
    |.:.|||. |.:|. |:.|.     ... ::: ..
149 VARPGTETSDVVCKPCAPGTFSNTTSSTDICRPHQICNVVAIPGNASMDA 198
```

Figure 8

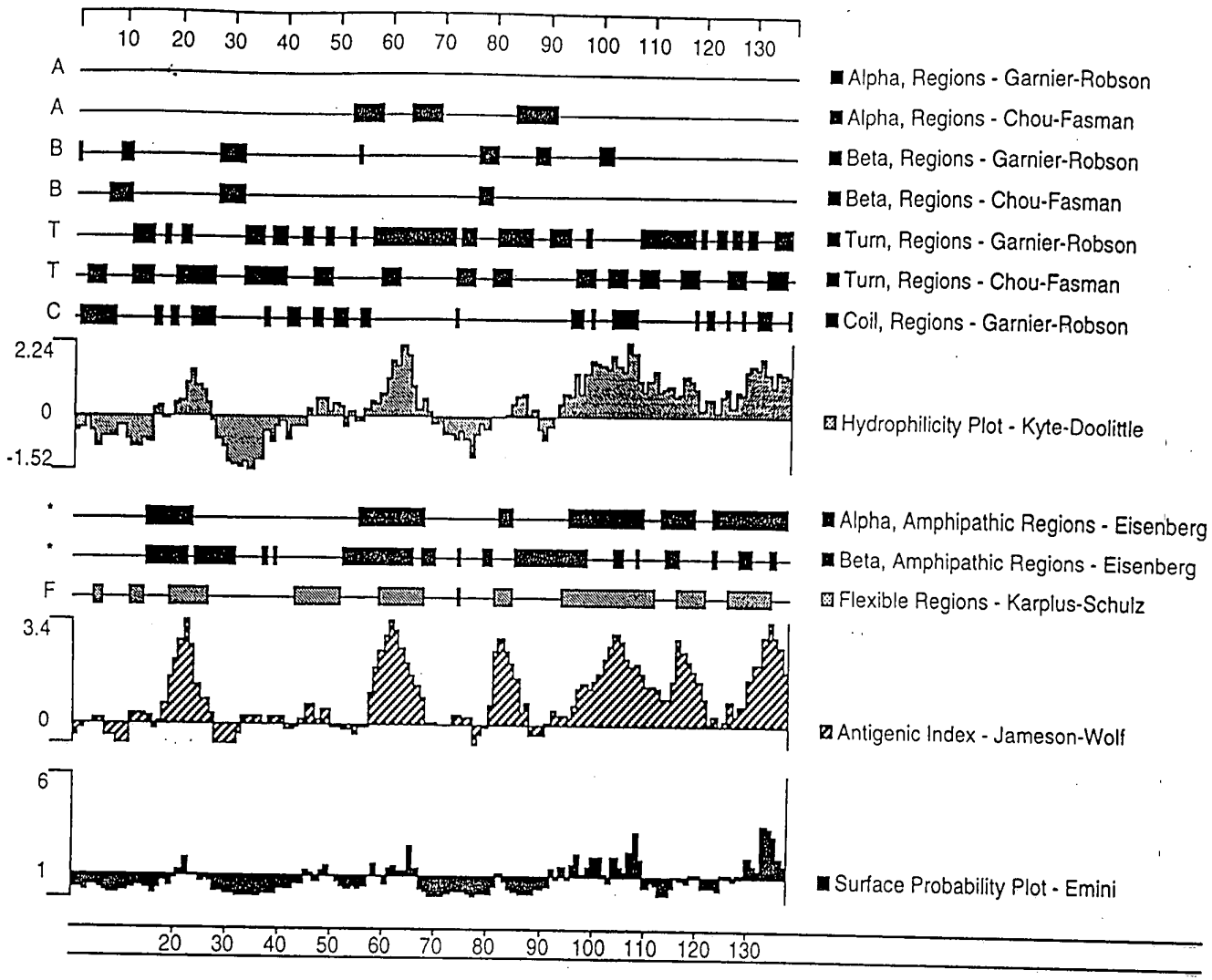

Figure 9

Percent Similarity: 73.370 Percent Identity: 59.783

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    |||||||||||||||||:||||||||||||||||||||||||||||||||
  1 MEPPGDWGPPPWRSTPRTDVLRLVLYLTFLGAPCYAPALPSCKEDEYPVG 50

 51 SECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKCLQCQMCD 100

101 PAMGLRAS.RNCSRTENAVCGCSPGHFCIVQDGDHCAACRAYATSSPGQR 149
    |.:| ... |. :: |.:       :|:: ..: :...:  |:.. |::.
101 PDIGSPCDLRGRGHLEAG......AHLSPGRQKGEPDPEVAFESLSAEPV 144

150 VQKGGTESQDTLCQNCPPGTFSPNGTLEECQHQTKCSWLVTKAGAGTSSS 199
      .|. . :. .. : ::. :..:.|.          | .:|::..::.
145 HAANGSVPLEPHARLSMASAPCGQAGLH.......LRDRADGTPGGR 184

200 HWVWWFLSGSLVIVIVCSTVGLIICVKRRKPRGDVVKVIVSVQRKRQEAE 249
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Figure 10

Percent Similarity: 70.588 Percent Identity: 60.294

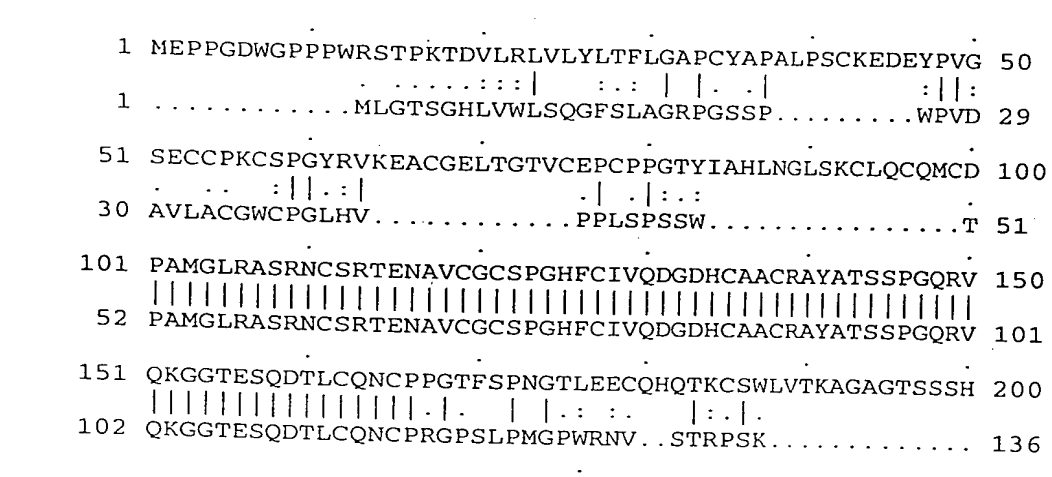

Figure 11

Percent Similarity: 37.984 Percent Identity: 20.155

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  1 ............MLGTSGHLVWLSQGFSLAGRPGSSPWPVDAVLACGWCP 38

 44 EDEYPVGSECCPKCSPGYRVKEACGELTGTVCEPCPPGTYIAHLNGLSKC 93
    : . |. |.:: ... |.|.. .|:   ...||:.:|.  :|  :.: ..|
 39 GLHVPPLSPSSWTPAMGLRASRNCSRTENAVCGCSPGHFCI..VQDGDHC 86

 94 LQCQMCDPDIGSPCDLRGRGHLEAGAHLSPGRQKGEPDPEVAFESLSAEP 143
    .|. :..  :||.:  .:|  |... |:.. .:|.. | .:: .:|. |
 87 AACRAYAT..SSPGQRVQKGGTESQDTLCQNCPRGPSLPMGPWRNVSTRP 134

144 VHAANGSVPLEPHARLSMASAPCGQAGLHLRDRADGTPGGRA. 185
                                                |
135 SK..................................................... 136
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Figure 12

Percent Similarity: 92.168 Percent Identity: 92.168

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  1 ........GCACGAGCTGCCTCCCGCAGGCGCCACCTGTGTCCCCCAGCG  42
                ||    |||||||  |||  ||||||||||||||  |||||||
101 TTGCCTGGACAGCTCCTGCCTCAGGCA.GCGCCACCTGTGTCGCCCAGCG 149

 43 CCGCTCCACCCAGCAGGCCTGAGCCCCTCTCTGCTGCCAGACACCCCCTG  92
    ||||||||||||||||||||||||||||||||||||||||||||||||||
150 CCGCTCCACCCAGCAGGCCTGAGCCCCTCTCTGCTGCCAGACACCCCCTG 199

 93 CTGCCCACT.CTCCTGCTGCTCGGGTTCTGAGGCACAGCTTGTCACACCG 141
    |||||||||  ||||||||||||||||||||||||||||||||||||||||
200 CTGCCCACTACTCCTGCTGCTCGGGTTCTGAGGCACAGCTTGTCACACCG 249

142 AGGCGGATTCTCTTTCTCTTTCTCTTTCTCTTCTGGCCCACAGCCGCAGC 191
    |||||||||||||||||||||||||||||||||||||||||||||||||||
250 AGGCGGATTCTCTTTCTCTTTCTCTTTCTCTTCTGGCCCACAGCCGCAGC 299

192 AATGGCGCTGAGTTCCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCCG 241
    |||||||||||||||||||||||||||||||||||||||||||||||||||
300 AATGGCGCTGAGTTCCTCTGCTGGAGTTCATCCTGCTAGCTGGGTTCCCG 349

242 AGCTGCCGGTCTGAGCCTGAGGCATGGAGCCTCCTGGAGACTGGGGGCCT 291
    ||||||||||||||||||||  ||||||||||||||||||||||||||||
350 AGCTGCCGGTCTGAGCCTGAGTCATGGAGCCTCCTGGAGACTGGGGGCCT 399

292 CCTCCCTGGAGATCCACCCCCAAAACCGACGTCTTGAGGCTGGTGCTGTA 341
    ||||||||||||||||||||  ||||||||||||||||||||||||||||
400 CCTCCCTGGAGATCCACCCCCAGAACCGACGTCTTGAGGCTGGTGCTGTA 449

342 TCTCACCTTCCTGGGAGCCCCCTGCTACGCCCCAGCTCTGCCGTCCTGCA 391
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
450 TCTCACCTTCCTGGGAGCCCCCTGCTACGCCCCAGCTCTGCCGTCCTGCA 499

392 AGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAGTGCAGTCCA 441
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
500 AGGAGGACGAGTACCCAGTGGGCTCCGAGTGCTGCCCCAAGTGCAGTCCA 549

442 GGTTATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGCACAGTGTGTGA 491
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
550 GGTTATCGTGTGAAGGAGGCCTGCGGGGAGCTGACGGGCACAGTGTGTGA 599

492 ACCCTGCCCTCCAGGCACCTACATTGCCCACCTCAATGGCCTAAGCAAGT 541
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
600 ACCCTGCCCTCCAGGCACCTACATTGCCCACCTCAATGGCCTAAGCAAGT 649

542 GTCTGCAGTGCCAAATGTGTGAC..........................  564
    |||||||||||||||||||||||
650 GTCTGCAGTGCCAAATGTGTGACCCAGATATTGGTTCCCCCTGTGACCTC 699


565 ..............CCAGCCATGGGCCTGCGCGCGAGCCGGAACTGCTC 599
                  ||||||||||||||||||||||||||||||||||||
1600 CCCTCCTCTTGGACTCCAGCCATGGGCCTGCGCGCGAGCCGGAACTGCTC 1649

600 CAGGACAGAGAACGCCGTGTGTGGTTGCAGCCCAGGCCACTTCTGCATCG 649
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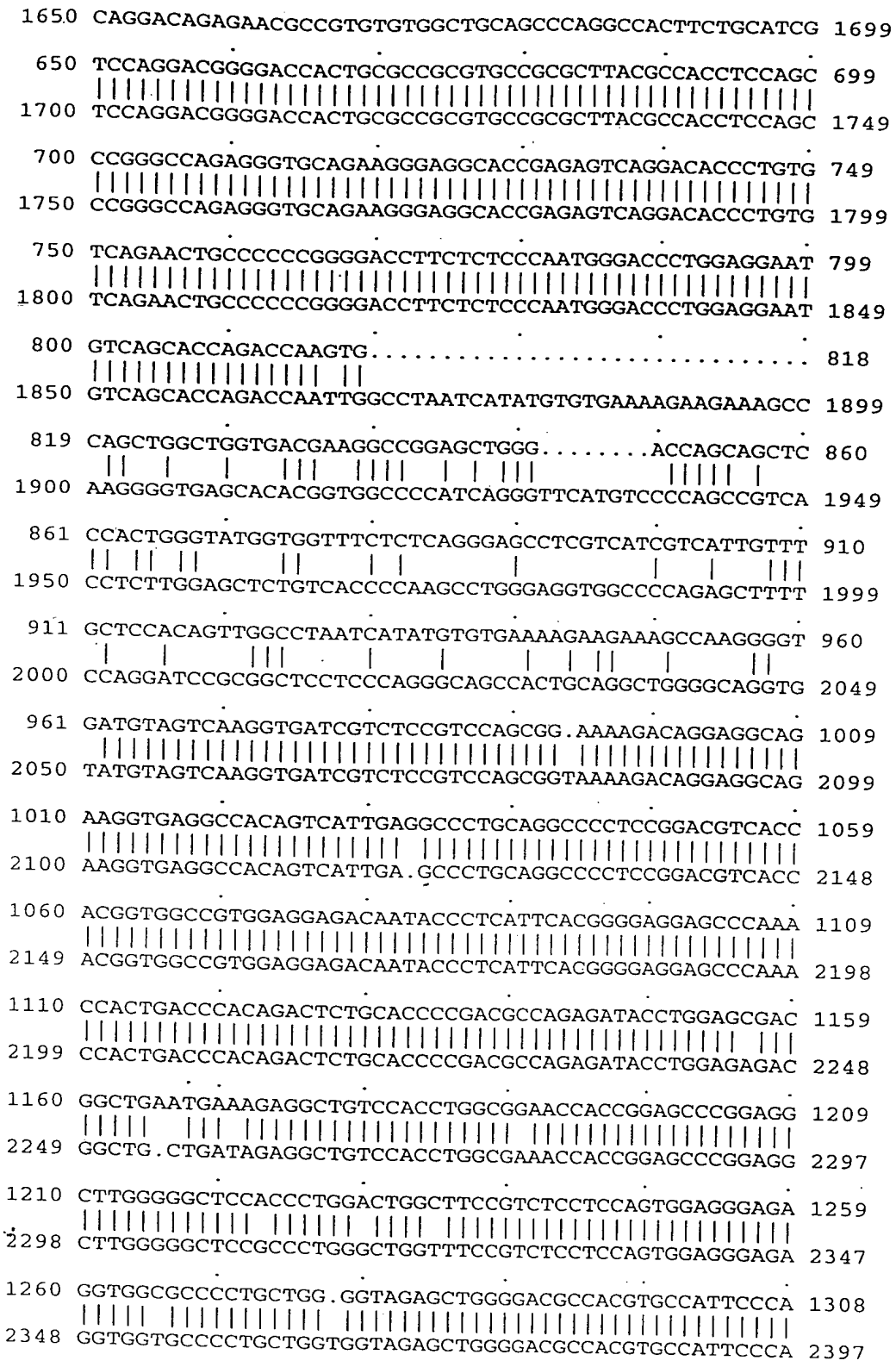
Figure 13A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800 GTCAGCACCAGACCAAGTG..... 818
1850 GTCAGCACCAGACCAATTGGCCTAATCATATGTGTGAAAAGAAGAAAGCC 1899
819 CAGCTGGCTGGTGACGAAGGCCGGAGCTGGG.....ACCAGCAGCTC 860
1900 AAGGGGTGAGCACACGGTGGCCCCATCAGGGTTCATGTCCCCAGCCGTCA 1949
861 CCACTGGGTATGGTGGTTTCTCTCAGGGAGCCTCGTCATCGTCATTGTTT 910
1950 CCTCTTGGAGCTCTGTCACCCCAAGCCTGGGAGGTGGCCCCAGAGCTTTT 1999
911 GCTCCACAGTTGGCCTAATCATATGTGTGAAAAGAAGAAAGCCAAGGGGT 960
2000 CCAGGATCCGCGGCTCCTCCCAGGGCAGCCACTGCAGGCTGGGGCAGGTG 2049
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2050 TATGTAGTCAAGGTGATCGTCTCCGTCCAGCGGTAAAAGACAGGAGGCAG 2099
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2100 AAGGTGAGGCCACAGTCATTGA.GCCCTGCAGGCCCCTCCGGACGTCACC 2148
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2149 ACGGTGGCCGTGGAGGAGACAATACCCTCATTCACGGGGAGGAGCCCAAA 2198
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2249 GGCTG.CTGATAGAGGCTGTCCACCTGGCGAAACCACCGGAGCCCGGAGG 2297
1210 CTTGGGGGCTCCACCCTGGACTGGCTTCCGTCTCCTCCAGTGGAGGGAGA 1259
2298 CTTGGGGGCTCCGCCCTGGGCTGGTTTCCGTCTCCTCCAGTGGAGGGAGA 2347
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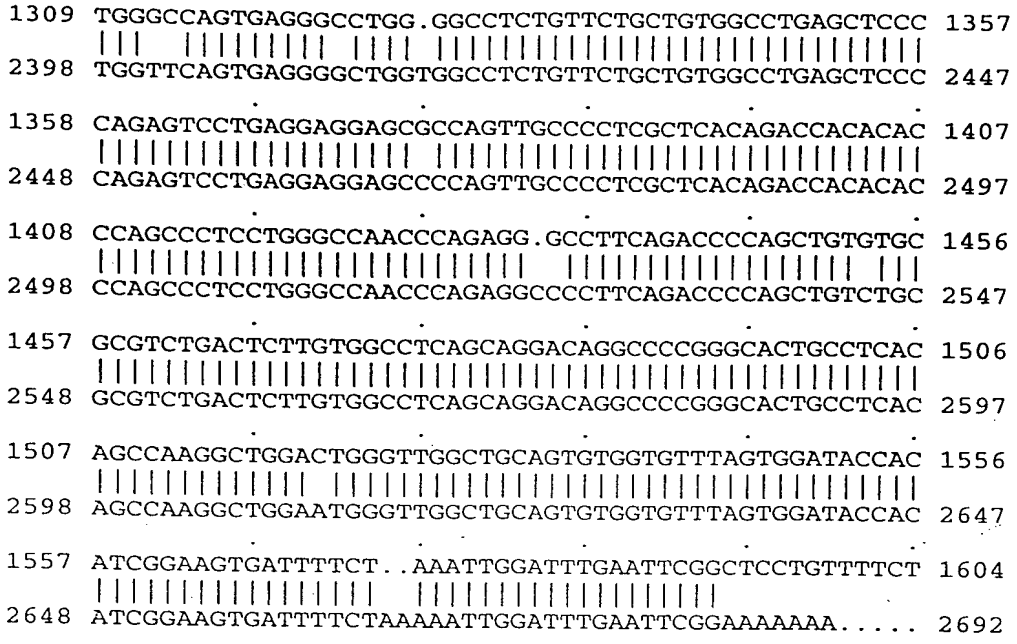
Figure 13B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2498 CCAGCCCTCCTGGGCCAACCCAGAGGCCCCTTCAGACCCCAGCTGTCTGC 2547
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2548 GCGTCTGACTCTTGTGGCCTCAGCAGGACAGGCCCCGGGCACTGCCTCAC 2597
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1557 ATCGGAAGTGATTTTCT..AAATTGGATTTGAATTCGGCTCCTGTTTTCT 1604
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Figure 13C

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   1 .........................GCACGAGCTGCCTCCCGCAGGCGC 24
 701 GTTGCTTCCCTGGGAGATGACCGTCTTCTCCAGCAGAAAGGTTGAAGGTC 750

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 751 CCACCCTGAGCGGCACCCTGGTCACATGCCTGCGTCCAGGAGAGCTGCAG 800

  75 GCTGCCAGACACCCCCTGCTGCCCACTCTCCTGCTGCTCGGGTTCTGAGG 124
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 851 CTCATCAGATCTGAGCTTCCTGGAGGCTCAGGATGGGCCTTCCCAGAAGC 900

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 901 AGGCCCAGAGGGAGGCTGCCTCCAGATCCCCTGTCCCCTGGGGCTGTGGG 950

 220 CATCCTGCTAGCTGGGTTCCCGAGCTGCCGGTCTGAGCCTGAGGCATGGA 269
 951 TGTCCCTGAATGTCAGGGCCATGGGAGGGCCCCTGGGCTTCAGGGGTTGG 1000

 270 GCCTCCTGGAGACTGGGGGCCTCCTCC.....CTGGAGATCCACCCCCAA 314
1001 GGAAAGTGAACACTCTGCTCTTTGTCCACCTTCGGGAGGACAACCTTCAA 1050

 315 A.......ACCGACGTCTTGAGGCTGGTGCTGTATCTCACCTTCCTGGGA 357
1051 ATGCTGACCCTGGGCCCCTAACTGACCTGAGACTTCAGAGCTTCTTGGGA 1100
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Figure 14A

```
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1101 GGAGCTGGGGTCCCCCAGCGGAGCCTGGGATGGAGCAGGGATGGCTGCCC 1150

 408 AGTGGGCTCCGAGTGCTGCCCCAAGTGCAGTCCAGGTTATCGTGTGAAGG  457
1151 CAGGGAGGGGGCGGTGGGGCCTTCCATCCTGCTCTGCCCTCCTCGTCCTC 1200

 458 AGG..CCTGCGGGGAGCTGACGGGCACAGTGTGTGAACCCTGCCCTCCAG  505
1201 TGGCCCCAGCTCAGTCCTGTCCATCTCCAGCTCTAACCATTTGTGGCCCG 1250

 506 GCACCTACATTGCCCACCTCAATGGCCTAAGCAAGTGTCTGCAGTGCC..  553
1251 ACACTGGCTCTCCCTCTACCTTCTGTCCTTGTCTGACACTGGTCTCCCGT 1300

 554 .AAATGTGTGACCCAGCCATGGCCTGCGCGCGAGCCGGAACTGCTCCAG  602
1301 GCTCTGGGGTCTCTGCACTGATGGCTGCCTCCCGCTTCTCTCCCCTCTCC 1350

 603 GACAGAGAACGCCGTGTGTGGTTGCAGCCCAGGCCACTTCTGCATCGTCC  652
1351 CTCTGCCGTCCTGTCTCCTGTGGCCAGTCTCTCCTTGTTTCTCTTCTCCT 1400

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1501 TGTCTTCACTGCCTGGGGCCCTGGGAGCCAGGGAGGCTCCCTGAGGCTGA 1550

 797 ....................................AATGTCAGCACCAG  810
1551 GTGAACACTGGGCGCTGCACCTGCCTCTCCCACGTCCTCGGCCCCACTCC 1600

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Figure 14B

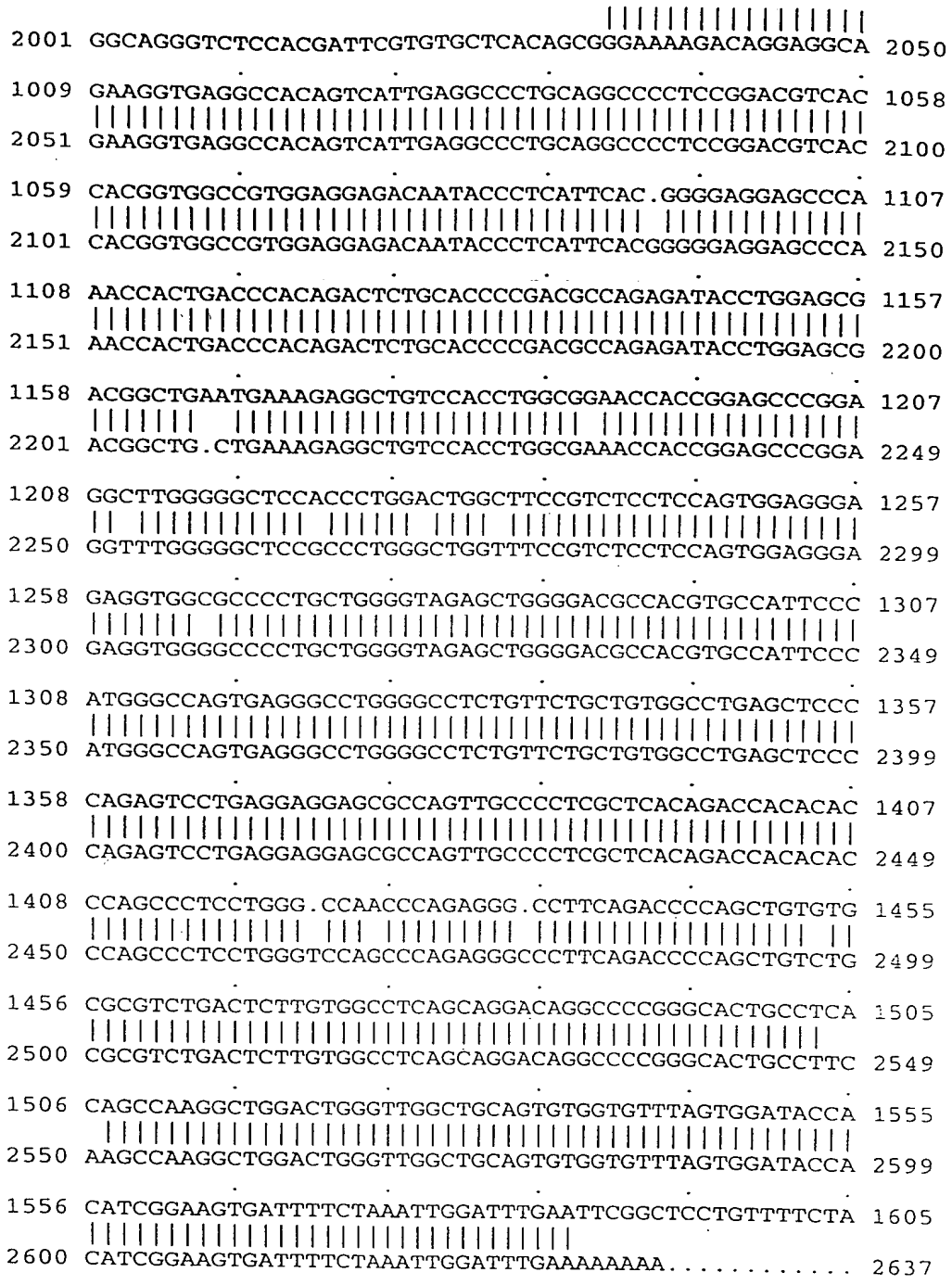
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Figure 14C

Percent Similarity: 53.479 Percent Identity: 53.479

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Figure 15A

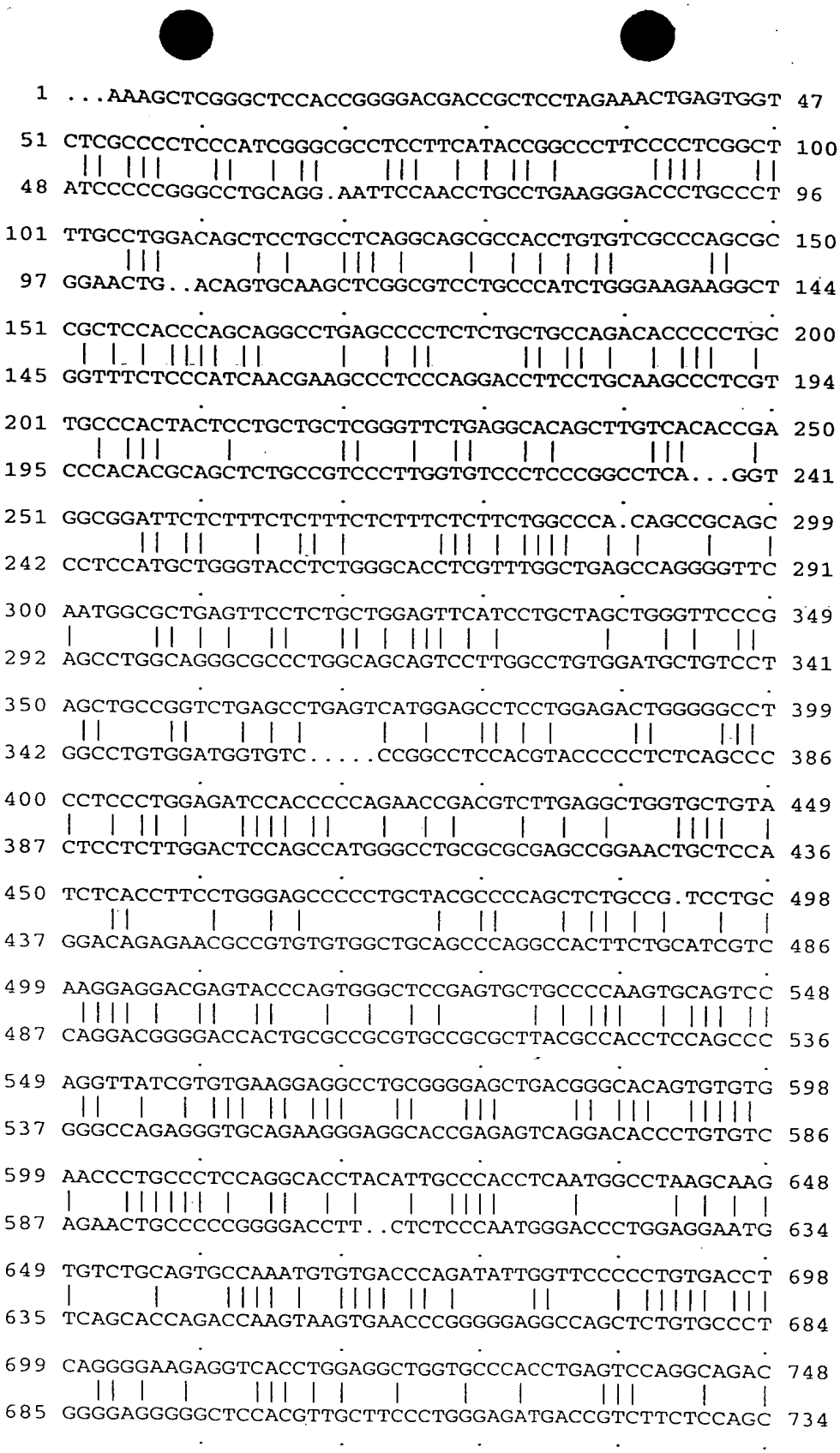
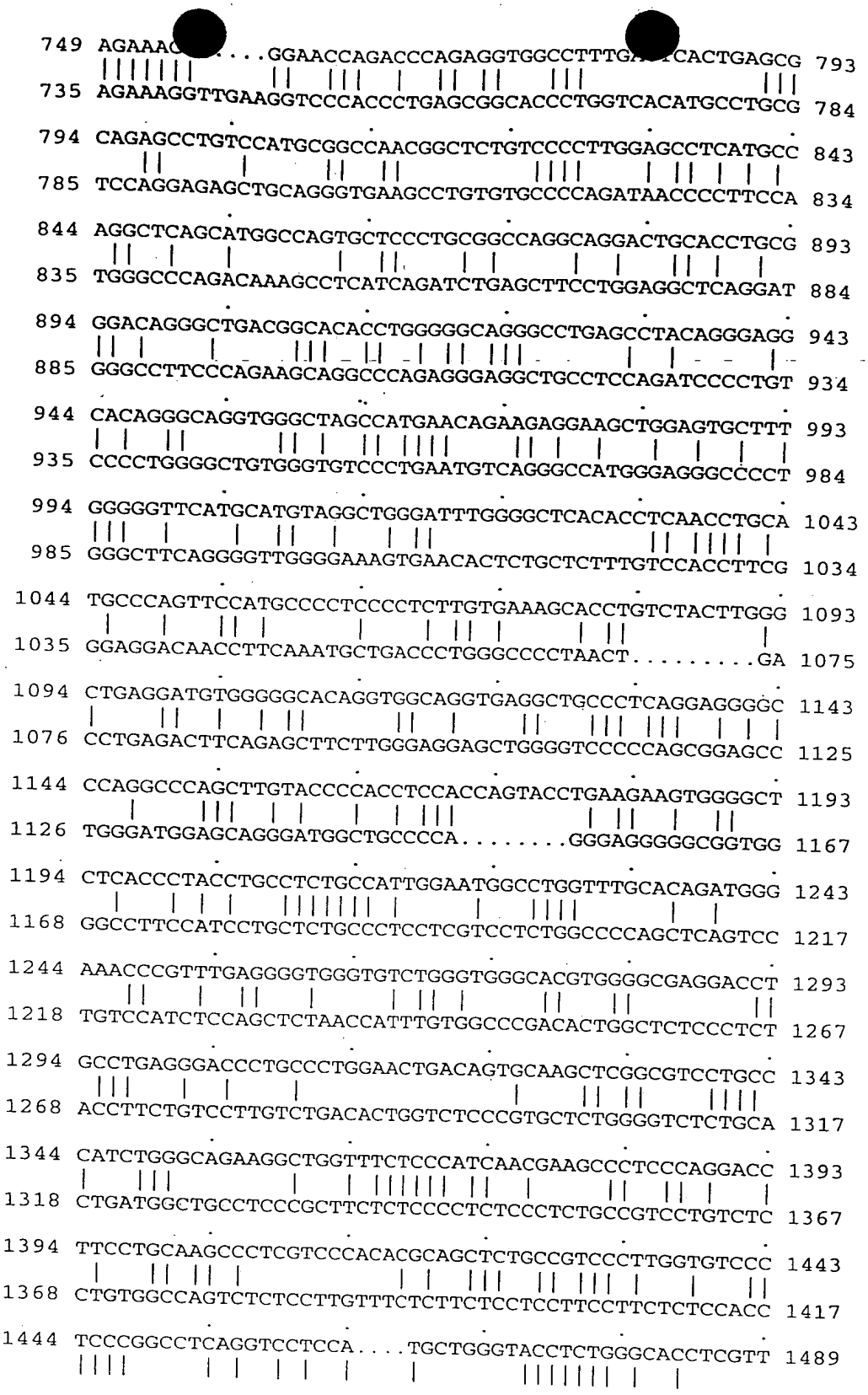


Figure 15B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1268 ACCTTCTGTCCTTGTCTGACACTGGTCTCCCGTGCTCTGGGGTCTCTGCA 1317
1344 CATCTGGGCAGAAGGCTGGTTTCTCCCATCAACGAAGCCCTCCCAGGACC 1393
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Figure 15C

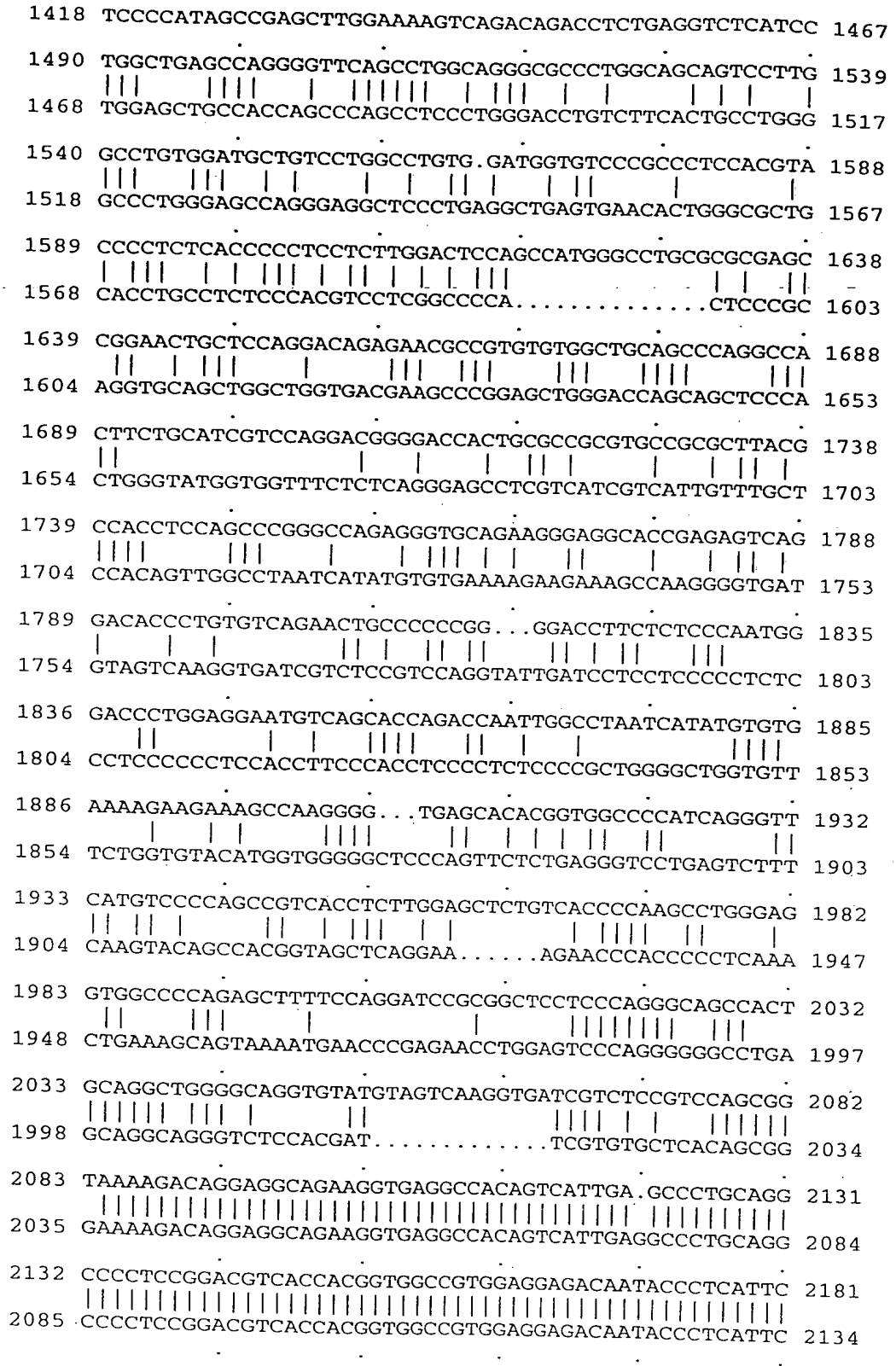
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Figure 15D

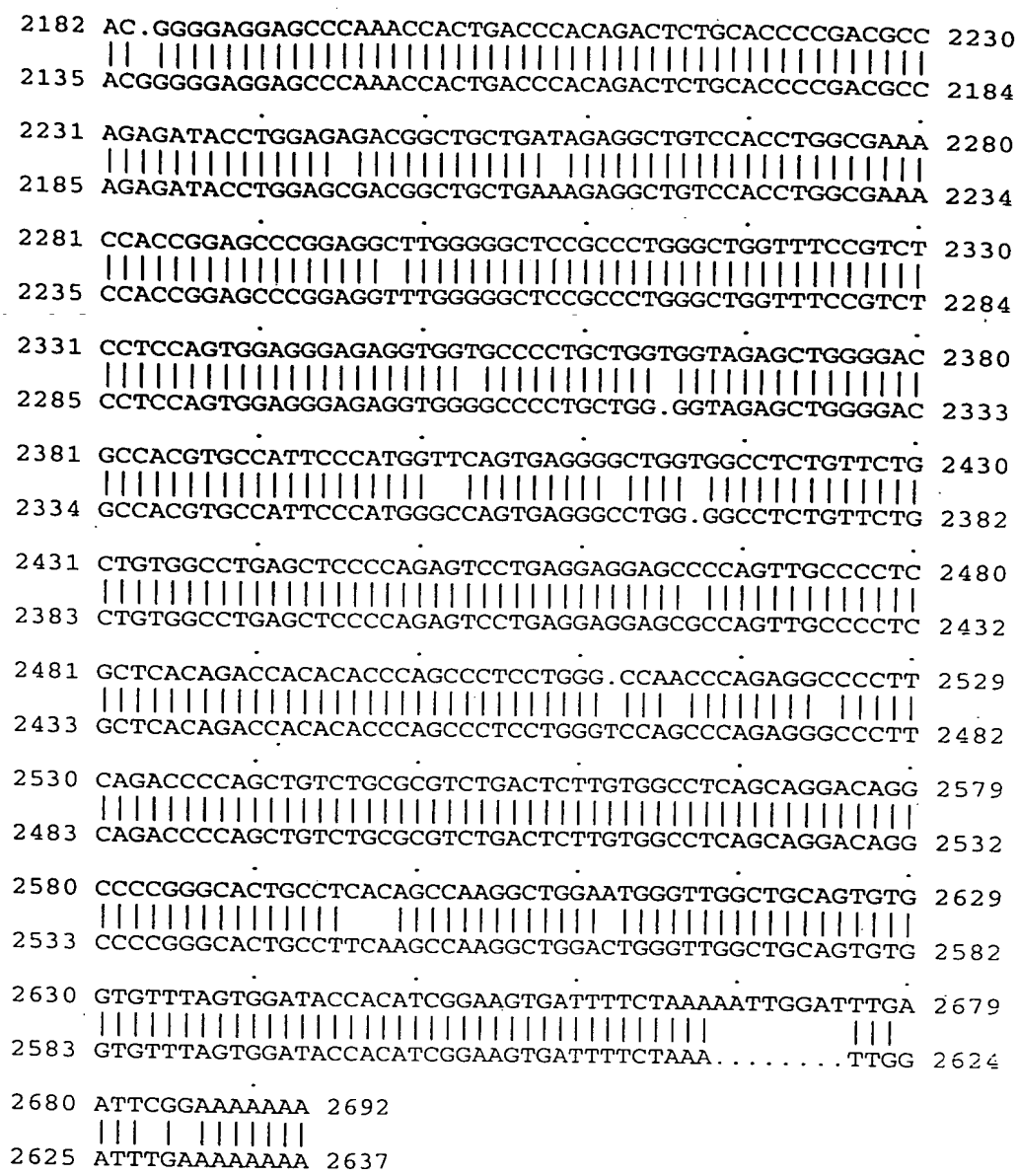
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Figure 15E

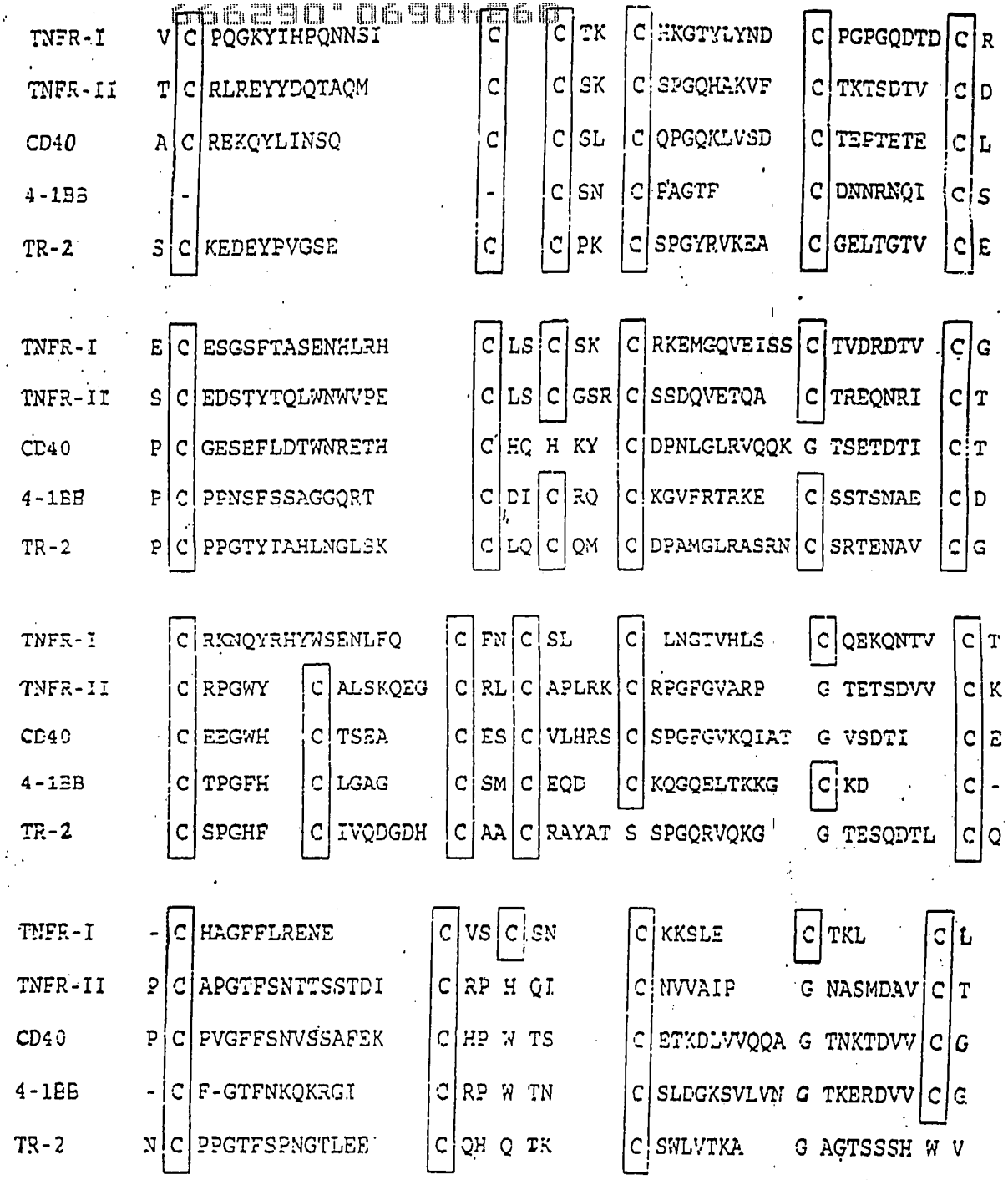

Figure 16